



Influence of Factors on the gastrointestinal microbiota of Pigs

M. Bolibrukh , I. Rublenko 

Bila Tserkva National Agricultural University, Soborna sq., 8/1, Bila Tserkva, 09111, Ukraine

Article info

Received 20.02.2023

Received in revised form
20.03.2023

Accepted 21.03.2023

Correspondence author

Iryna Rublenko

Tel.: +38-097-398-57-83

E-mail: rublenkoi@meta.ua

2023 Bolibrukh M. and Rublenko I. This is an open-access article distributed under the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.



Contents

1. Introduction	68
2. Results and discussion	68
2.1 Results	68
2.2 Discussion	69
3. Conclusions	70
References	70

Abstract

A complete understanding of the dynamic distribution of the intestinal microbiota in pigs is essential because microorganisms play a fundamental role in physiological processes, immunity, and nutrient metabolism by the macroorganism. Disruption of the gut microbiome can cause inflammation, oxidative stress, and a cytokine storm. Gut microbiome dysfunction can be caused by short-term or long-term (environmental, nutritional, and stress) factors. The microbial ecosystem of the intestine is fundamental for the pig's proper nutrition, and physiological and immunological functions. However, the composition and function of a healthy microbial ecosystem have yet to be qualitatively and quantitatively determined to be used as a tool to maximize animal health and performance. As efforts are made to reduce the use of antibiotics in pig farming, the ability of the gut microbiota to increase disease resistance must be recognized. Generally, the genera *Bacteroides*, *Escherichia*, *Clostridium*, *Lactobacillus*, *Fusobacterium*, and *Prevotella* dominate in pre-weaning piglets. Then *Prevotella* and *Aneriacter* become the dominant genera, with *Fusobacterium*, *Lactobacillus* and Miscellaneous as relative minors in post-weaning piglets. Specific genera of bacteria, including *Bacteroides*, *Prevotella*, and *Lactobacillus*, can be detected in more than 90 % of pigs and three enterotypes – identified in animals of the same species but of different ages. This suggests the presence of a “core” microbiota in the gut of healthy pigs that may be a potential target for nutritional or health regulation. The scientists' scientific data help to determine the “optimal” gut microbial profile for evaluating or improving the performance and health status of pigs at different stages of growth. Although external and stochastic factors contribute to the individuality of the microbiota, the fundamental principles governing how environmental factors and host genetic factors combine to shape this complex ecosystem are largely unknown and require systematic study.

Keywords: pigs, intestinal microbiota, gut, bacteria, microflora composition, health.

Citation:

Bolibrukh, M., & Rublenko, I. (2023). Influence of Factors on the gastrointestinal microbiota of Pigs. *Ukrainian Journal of Veterinary and Agricultural Sciences*, 6(1), 68–71.

1. Introduction

Similar to humans, pigs have a complex and diverse community of microorganisms in the gastrointestinal tract (GIT) that play a fundamental role in immunity, physiological processes, and nutrient metabolism. The diversity, composition, and function of the gut microbial community depend on various factors, including diet, age, stress, and environment (Benson et al., 2010). This may directly or indirectly affect the host's metabolism, immune response, and intestinal homeostasis (David et al., 2014; Zhang et al., 2017), creating a so-called “cross-talk” between the gut microbiota and the macroorganism (Wylensek et al., 2020). Although the gut microbiota is considered an essential metabolic 'organ,' the microorganisms in the gastrointestinal tract of pigs have been studied less frequently than in humans. Research Fohse J. M., Zijlstra R. T., and Willing B. P. (2016) focused on a collection of cultured bacteria from the porcine gastrointestinal tract and revealed very distinct taxonomic groups with distinct metabolic functions, suggesting that the

understanding of the pig gut microbiota is less complete. Therefore, this issue is relevant for further study.

The research aimed to study the influence of factors (age, days of weaning, feed, etc.) on the composition of the microbiota of the gastrointestinal tract of pigs.

Publications of scientists served as **material for research**.

2. Results and discussion

2.1 Results

Age is an essential factor contributing to the maturation of the intestinal microbiota (Kim et al., 2012; Lin et al., 2018). The diversity of microbes in the gastrointestinal tract of pigs changes over time (Soler et al., 2018), and it can be assumed that the dynamic distribution of intestinal microbiota in pigs is represented along the longitudinal age axis (Li et al., 2017). Newborn animals have a critical period. During which microbial colonization occurs- when the microbiota structure is unstable and sensitive to environmental

conditions. There is growing evidence that early colonization of “appropriate” microorganisms can determine gut microbial composition and immunological maturation (Liang et al., 2018). Microbes are believed not to colonize the gastrointestinal tract of piglets before birth. However, bacterial populations immediately enter the gastrointestinal tract immediately after the animal is born. This process is mainly influenced by the sow (Slifierz et al., 2015), colostrum (Li et al., 2020), skin and feces, etc. Therefore, the fecal microbial community of suckling piglets is similar to that of their mother (Huang et al., 2019). Recent studies show that the early establishment of a stable gut microbiome plays a fundamental role in the development of the physiological function of the gastrointestinal tract and the maturation of the innate immune system after weaning, which directly affects the growth performance of growing and finishing pigs (Mu et al., 2017).

The development of intestinal microbiota in piglets is gradual and consistent (Li et al., 2020). In the first week after birth, *Bacteroides*, *Escherichia*, and *Clostridium* are the three most common genera of microorganisms. A marked shift from *Bacteroides* to *Prevotella* was observed as piglets aged/grew (Huang et al., 2019). Just two weeks after birth, *Prevotella* becomes the third dominant genus in the gut of piglets and increases to become the most abundant genus at weaning (21 days). In modern pig farming, piglets receive commercial feed 3–5 days after birth. The transition from the sow to solid feed helps to form the microbiota of the gastrointestinal tract of piglets.

Prevotella is associated with increased long-term carbohydrate intake (Kaevska et al., 2016) and can metabolize complex dietary polysaccharides (Liu et al., 2017). In solid feed consumption, bacteria such as *Prevotella* gradually take a dominant position. In addition, other genera such as *Blautia* (Mu et al., 2017; Liang et al., 2018), *Paraprevotella*, *Oscillibacter*, *Roseburia*, *Ruminococcus*, *Oscillospira*, *Coproccoccus*, *Faecalibacterium* and *Treponema* (Kaevska et al., 2016; Liang et al., 2018) increase in large quantities in the intestines of piglets in the period from birth to weaning. However, such genera of microorganisms as *Bacteroides* (Kaevska et al., 2016; Liang et al., 2018), *Parabacteroides* (Zhang et al., 2016), *Fusobacterium* (Kaevska et al., 2016; Mu et al., 2017; Liang et al., 2018), *Lactobacillus* (Looft et al., 2014), *Anaerotruncus* (Liang et al., 2018), *Butyrivibrio* (Liang et al., 2018), *Streptococcus* (Kaevska et al., 2016; Liang et al., 2018), *Clostridium* and *Escherichia* – decrease (Kaevska et al., 2016).

As pigs grow, the diversity and richness of microbiota in the intestines increase. According to a large number of studies, *Prevotella* spp. are the most common bacteria in the gastrointestinal tract of pigs at the age of 28 to 91 days, but their number decreases at the age of 91 to 154 days (Looft et al., 2014; Li et al., 2017) – the proportion of bacteria *Anaerobacter* spp. increases when pigs grow, becoming the most common type of bacteria in the GIT at 154 days (Looft et al., 2014). Over time, other bacteria such as *Lactobacillus*, *Fusobacterium*, *Oscillospira*, *Escherichia*, *Roseburia*, *Faecalibacterium*, and *Bacteroides* are also part of the dominant microbiota in the pig gut during the growing period. During this period, feed consumption and the body weight of pigs increase sharply. At the same time, this functional composition of the intestinal microbiota can reduce the risk of infectious intestinal diseases and ensure the full realization of the growth potential of animals.

Defining the “core microbiome” in the pig gut has been the focus of numerous publications (Poulsen et al., 2018), which is intriguing as it may provide new targets for medical, dietary, or therapeutic interventions. Based on mean relative abundance, microbial representatives with high abundance throughout life can be accepted as part of the “core” microbiome of the pig gut. On the other hand, microbial species that appear in pigs' gastrointestinal tract only at specific growth stages are proposed to be considered a “stage-associated” microbiome (Kaevska et al., 2016).

Although a “core” microbiota may not exist in pigs according to a strict definition, the scientists still found several types and genera of bacteria, in more than 90 % of the samples, at all stages of growth. Bacteria of the genus *Firmicutes* and *Bacteroidetes* accounted for the majority of total sequences (72.93 % in weanling piglets, 89.32 % in post-weaning piglets, 89.78 in rearing piglets and 87.42 % in fattening piglets).

It has been established that more than 90 % of pigs contain bacteria of 19 genera, defined as “main”. Accordingly, *Bacteroides*, *Escherichia*, and *Lactobacillus* predominate in weanling piglets, while *Prevotella*, *Lactobacillus*, and *Oscillospira* predominate in post-weaning piglets. In growing animals, the three most common genera are *Prevotella*, *Lactobacillus*, and *Faecalibacterium*, and in fattening animals, *Prevotella*, *Lactobacillus*, and *Streptococcus*.

These dominant bacterial taxa may be potential functional microbiota not only because of their relatively high abundance but also because of their greater frequency of contact with the host's intestinal mucosa. Further studies of these “main” microbes and their dynamic distribution, as well as the associated function, are of great importance for pig farming, as they impact the daily weight gain of animals and their physiological state (Looft et al., 2014).

Since the 1950s, antibiotics have been used as a growth factor in pigs and for therapeutic purposes. However, their effect on changing the microbial composition is variable: treatment with tiamulin and chlortetracycline for 14 days in newborns significantly increased the amount of IgA, while carbadox and oxytetracycline did not change (Hazon, 2019). The use of antibiotics as a supplement did not cause significant changes in IgG or IgA E in fattening animals. Since 2006, the European Union has banned antibiotics as growth promoters. Furthermore, more recently, in 2018, he passed a law on reducing the prophylactic use of antibiotics. Indeed, due to the systematic use of antibiotics in animal husbandry, the problem of the development of antibiotic resistance has arisen (Fleury, 2015).

Scientist Mickaël Fleury, while studying the assessment of the effect of antibiotics on the intestinal microbiota of piglets (colistin and ceftiofur), established resistance to antibiotics that caused chromosomal mutations and changes in gene plasmids. In particular, colistin significantly reduced the population of enterobacteria but, at the same time, did not cause resistance in *E. coli*. The administration of ceftiofur to pigs affected the bacterial populations of the digestive ecosystem but, at the same time, led to the selection and diffusion of the plasmid gene encoding beta-lactamase in bacteria (Yu et al., 2017).

2.2 Discussion

Various scientists have debated the relationship between performance and gut microbiota in pigs in recent years. It has been reported that birth weight strongly affects the bac-

terial composition of the gastrointestinal tract of piglets from 7 to 21 days (Yu et al., 2017). In addition, a link between body weight and the microbial composition of the intestines of pigs was found. For example, the levels of *Bacteroides* (2.65 % vs. 4.54 %), *Anaerotruncus* (0.01 % vs. 0.03 %), and *Anaerococcus* (0.02 % vs. 0.01 %) were significantly different in guts with larger masses (from 16.70 to 22.75 kg) of pigs than with a smaller one (from 8.09 to 11.89 kg) (Liu et al., 2017). It was also found that the body weight of pigs at the age of 136 days is positively correlated with the number of the microbiota of the genus Firmicutes and negatively correlated with *Bacteroidetes* (Xu et al., 2016).

Increasing evidence suggests that the gut microbiota may play an essential role in regulating appetite and feeding behavior in pigs. A correlation was found between enterotypes and food consumption by animals of this species at the stage of completion of fattening (Looft et al., 2014). For example, pigs with a *Prevotella*-dominated enterotype consume more food than *Treponema*-dominated pigs (Kaevska et al., 2016). This indicates that microorganisms of the genus *Prevotella* may be the key and a potential new target for increasing food consumption. How the gut microbiota affects appetite in pigs remains unknown, but studies in other animal models may provide valuable clues (Slifierz et al., 2015).

Various factors affect the gastrointestinal microflora. In particular, antibiotics that are currently used for therapeutic purposes. To better assess the impact and quality of antibiotic therapy on animals, international organizations publish recommendations to reduce the use of antibiotics (WOAH) and “continue monitoring the sale of antibiotics and exposure to them by creating an observatory of use within the framework of Anses-NAVIM (National Agency of Veterinary Medicine) to analyze the data on medicated feed further”, “introduce a regular survey of representative veterinarians and farmers and extend pharmaco-epidemiological studies to all sectors”. At the European level, this goal is part of an approach coordinated by the European Medicines Agency within the ESVAC (European Surveillance of Veterinary Antimicrobial Use) project. The problem of studying the effect of antibiotics on the microflora of the gastrointestinal tract of pigs and other animals still needs to be solved and relevant (Dewulf et al., 2022).

3. Conclusions

Thus, it was established that age and feeding are important factors influencing the intestinal microbiota of pigs. The most common genera of bacteria are *Bacteroides*, *Escherichia*, *Clostridium*, *Lactobacillus*, *Fusobacterium*, and *Prevotella*. These microorganisms dominate in piglets before weaning. Over time, they change, depending on age and feeding, to the predominance of *Prevotella* and *Aneriacter*. After weaning, the genera *Fusobacterium*, *Lactobacillus*, and *Miscellaneous* are also the dominant microflora in piglets.

Conflict of interests

The authors (M. Bolibrukh, I. Rublenko) of the article “Influence of factors on the gastrointestinal microbiota of pigs” state that there is no conflict of interest regarding their contribution and the study results.

References

- Benson, A. K., Kelly, S. A., Legge, R., Ma, F., Low, S. J., Kim, J., Zhang, M., Oh, P. L., Nehrenberg, D., Hua, K., Kachman, S. D., Moriyama, E. N., Walter, J., Peterson, D. A., & Pomp, D. (2010). Individuality in gut microbiota composition is a complex polygenic trait shaped by multiple environmental and host genetic factors. *Proceedings of the National Academy of Sciences of the United States of America*, 107(44), 18933–18938. [\[Crossref\]](#) [\[Google Scholar\]](#)
- David, L. A., Maurice, C. F., Carmody, R. N., Gootenberg, D. B., Button, J. E., Wolfe, B. E., Ling, A. V., Devlin, A. S., Varma, Y., Fischbach, M. A., Biddinger, S. B., Dutton, R. J., & Turnbaugh, P. J. (2014). Diet rapidly and reproducibly alters the human gut microbiome. *Nature*, 505, 559–563. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Dewulf, J., Joosten, P., Chantziaras, I., Bernaerdt, E., Vanderhaeghen, W., Postma, M., & Maes, D. (2022). Antibiotic Use in European Pig Production: Less Is More. *Antibiotics*, 11(11), 1493. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Fleury, M. (2015). Impact de traitements antibiotiques sur la flore digestive du porcelet: Etude in vivo et développement d’une approche en système de fermentation in vitro. Médecine humaine et pathologie. Université de Rennes. Français. [\[Document\]](#) [\[Google Scholar\]](#)
- Fouhse, J. M., Zijlstra, R. T., & Willing, B. P. (2016). The role of gut microbiota in the health and disease of pigs. *Animal Frontiers*, 6(3), 30–36. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Huang, A., Cai, R., Wang, Q., Shi, L., Li, C., & Yan, H. (2019). Dynamic change of gut microbiota during porcine epidemic diarrhoea virus infection in suckling piglets. *Frontier in Microbiology*, 10, 322. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Kaevska, M., Lorencova, A., Videnska, P., Sedlar, K., Provaznik, I., & Trckova, M. (2016). Effect of sodium humate and zinc oxide used in prophylaxis of post-weaning diarrhoea on faecal microbiota composition in weaned piglets. *Veterinarni Medicina*, 61(6), 328–336. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Kim, H. B., Borewicz, K., White, B. A., Singer, R. S., Sreevatsan, S., Tu, Z. J., & Isaacson, R. E. (2012). Microbial shifts in the swine distal gut in response to the treatment with antimicrobial growth promoter, tylosin. *Proceedings of the National Academy of Sciences of the United States of America*, 109(38), 15485–15490. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Li, H., Liang, T., Chu, Q., Xu, F., Li, Y., Fu, L., & Zhou, B. (2017). Effects of several in-feed antibiotic combinations on the abundance and diversity of fecal microbes in weaned pigs. *Canadian Journal of Microbiology*, 63(5), 402–410. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Li, Y., Wang, X., Wang, X-q., Wang, J., & Zhao, J. (2020). Life-long dynamics of the swine gut microbiome and their implications in probiotics development and food safety. *Gut Microbes*, 11, 1824–1832. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Liang, H., Dai, Z., Liu, N., Ji, Y., Chen, J., Zhang, Y., Yang, Y., Li, J., Wu, Z., & Wu, G. (2018). Dietary L-tryptophan modulates the structural and functional composition of the intestinal microbiome in weaned piglets. *Frontiers in Microbiology*, 9, 1736. [\[Crossref\]](#) [\[Google Scholar\]](#)
- Lin, C., Wan, J., Su, Y., & Zhu, W. (2018). Effects of early intervention with maternal fecal microbiota and antibiotics on the gut microbiota and metabolite profiles of piglets. *Metabolites*, 8(4), 89. [\[Crossref\]](#) [\[Google Scholar\]](#)

- Liu, C., Zhang, C., Lv, W., Chao, L., Li, Z., Shi, D., & Guo, S. (2017). Structural modulation of gut microbiota during alleviation of suckling piglets' diarrhoea with herbal formula. *Evidence-Based Complementary and Alternative Medicine*, 2017, 1–11.
[Crossref] [Google Scholar]
- Looft, T., Allen, H. K., Cantarel, B. L., Levine, U. Y., Bayles, D. O., Alt, D. P., Henrissat, B., & Stanton, T. B. (2014). Bacteria, phages and pigs: the effects of in-feed antibiotics on the microbiome at different gut locations. *ISME Journal*, 8, 1566–1576.
[Crossref] [Google Scholar]
- Looft, T., Allen, H. K., Casey, T. A., Alt, D. P., & Stanton, T. B. (2014). Carbadox has both temporary and lasting effects on the swine gut microbiota. *Frontier in Microbiology*, 5, 276.
[Crossref] [Google Scholar]
- Hazon M. L. S. (2019). Microbiote intestinale chez le porc, facteurs de variation et relations avec les performances des animaux. Biologie animale. Agrocampus Ouest, Français. NNT: 2019NSARB323ff.
[Document] [Google Scholar]
- Mu, C., Yang, Y., Su, Y., Zoetendal, E. G., & Zhu, W. (2017). Differences in microbiota membership along the gastrointestinal tract of piglets and their differential alterations following an early-life antibiotic intervention. *Frontier in Microbiology*, 8, 797.
[Crossref] [Google Scholar]
- Poulsen, A. R., Jonge, N., Nielsen, J. L., Hojberg, O., Lauridsen, C., Cutting, S. M., & Canibe, N. (2018). Impact of *Bacillus* spp. spores and gentamicin on the gastrointestinal microbiota of suckling and newly weaned piglets. *PLoS One*, 13, e0207382.
[Crossref] [Google Scholar]
- Slifierz, M. J., Friendship, R. M., & Weese, J. S. (2015). Longitudinal study of the early-life fecal and nasal microbiotas of the domestic pig. *BMC Microbiology*, 15, 184.
[Crossref] [Google Scholar]
- Soler, C., Goossens, T., Bermejo, A., Migura-Garcia, L., Cusco, A., Francino, O., & Fraile, L. (2018). Digestive microbiota is different in pigs receiving antimicrobials or a feed additive during the nursery period. *PLoS One*, 13, e0197353.
[Crossref] [Google Scholar]
- Wylensek, D., Hitch, T. C. A., Riedel, T., Afrizal, A., Kumar, N., Wortmann, E., Liu, T., Devendran, S., Lesker, T. R., Hernandez, S. B., Heine, V., Buhl, E. M., Cumbo, F., Fischoder, T., Wyschkon, M., Looft, T., Parreira, V. R., Abt, B., Doden, H. L., Ly, L., Alves, J. M. P., Reichlin, M., Flisikowski, K., Suarez, L. N., Neumann, A. P., Suen, G., de Wouters, T., Rohn, S., Lagkouvardos, I., Allen-Vercoe, E., Sproer, C., Bunk, B., Taverne-Thiele Aj Giesbers, M., Wells, J. M., Neuhaus, K., Schnieke, A., Cava, F., Segata, N., Elling, L., Strowig, T., Ridlon, J. M., Gulder, T. A. M., Overmann, J., & Clavel, T. (2020). A collection of bacterial isolates from the pig intestine reveals functional and taxonomic diversity. *Nature Communication*, 11, 6389.
[Crossref] [Google Scholar]
- Xu, J., Chen, X., Yu, S., Su, Y., & Zhu, W. (2016). Effects of early intervention with sodium butyrate on gut microbiota and the expression of inflammatory cytokines in neonatal piglets. *PLoS One*, 11, 1–20.
[Crossref] [Google Scholar]
- Yu, T., Wang, Y., Chen, S., Hu, M., Wang, Z., Wu, G., Ma, X., Chen, Z., & Zheng, C. (2017). Low-molecular-weight chitosan supplementation increases the population of *Prevotella* in the cecal contents of weanling pigs. *Frontier in Microbiology*, 8, 2182.
[Crossref] [Google Scholar]
- Zhang, D., Ji, H., Liu, H., Wang, S., Wang, J., & Wang, Y. (2016). Changes in the diversity and composition of gut microbiota of weaned piglets after oral administration of lactobacillus or an antibiotic. *Applied Microbiology and Biotechnology*, 100(23), 10081–10093.
[Crossref] [Google Scholar]
- Zhang, M., Sun, K., Wu, Y., Yang, Y., Tso, P., & Wu, Z. (2017). Interactions between intestinal microbiota and host immune response in inflammatory bowel disease. *Frontiers in Immunology*, 8, 942.
[Crossref] [Google Scholar]